

David E Wentworth

List of Publications by Year in descending order

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68
papers

4,611
citations

109264

35
h-index

106281

65
g-index

70
all docs

70
docs citations

70
times ranked

6709
citing authors

#	ARTICLE	IF	CITATIONS
1	Intranasal powder live attenuated influenza vaccine is thermostable, immunogenic, and protective against homologous challenge in ferrets. <i>Npj Vaccines</i> , 2021, 6, 59.	2.9	9
2	Susceptibility of widely diverse influenza A viruses to PB2 polymerase inhibitor pimodivir. <i>Antiviral Research</i> , 2021, 188, 105035.	1.9	15
3	Detection of baloxavir resistant influenza A viruses using next generation sequencing and pyrosequencing methods. <i>Antiviral Research</i> , 2020, 182, 104906.	1.9	13
4	Integrating genotypes and phenotypes improves long-term forecasts of seasonal influenza A/H3N2 evolution. <i>ELife</i> , 2020, 9, .	2.8	35
5	Comparison of nucleic acid extraction methods for next-generation sequencing of avian influenza A virus from ferret respiratory samples. <i>Journal of Virological Methods</i> , 2019, 270, 95-105.	1.0	3
6	Ecosystem Interactions Underlie the Spread of Avian Influenza A Viruses with Pandemic Potential. <i>PLoS Pathogens</i> , 2016, 12, e1005620.	2.1	48
7	Molecular Characterizations of Surface Proteins Hemagglutinin and Neuraminidase from Recent H5Nx Avian Influenza Viruses. <i>Journal of Virology</i> , 2016, 90, 5770-5784.	1.5	52
8	Implementation of new approaches for generating conventional reassortants for live attenuated influenza vaccine based on Russian master donor viruses. <i>Journal of Virological Methods</i> , 2016, 227, 33-39.	1.0	11
9	Evolutionary Dynamics of Influenza A Viruses in US Exhibition Swine. <i>Journal of Infectious Diseases</i> , 2016, 213, 173-182.	1.9	28
10	Comparative <i>In Vitro</i> and <i>In Vivo</i> Studies of Porcine Rotavirus G9P[13] and Human Rotavirus Wa G1P[8]. <i>Journal of Virology</i> , 2016, 90, 142-151.	1.5	19
11	Genetically Diverse Low Pathogenicity Avian Influenza A Virus Subtypes Co-Circulate among Poultry in Bangladesh. <i>PLoS ONE</i> , 2016, 11, e0152131.	1.1	41
12	Adaptation of Pandemic H2N2 Influenza A Viruses in Humans. <i>Journal of Virology</i> , 2015, 89, 2442-2447.	1.5	29
13	H7N9 influenza A virus in turkeys in Minnesota. <i>Journal of General Virology</i> , 2015, 96, 269-276.	1.3	12
14	Evolution of Influenza B Virus in Kuala Lumpur, Malaysia, between 1995 and 2008. <i>Journal of Virology</i> , 2015, 89, 9689-9692.	1.5	10
15	Spread and Persistence of Influenza A Viruses in Waterfowl Hosts in the North American Mississippi Migratory Flyway. <i>Journal of Virology</i> , 2015, 89, 5371-5381.	1.5	29
16	Equine and Canine Influenza H3N8 Viruses Show Minimal Biological Differences Despite Phylogenetic Divergence. <i>Journal of Virology</i> , 2015, 89, 6860-6873.	1.5	36
17	Influenza A virus evolution and spatio-temporal dynamics in Eurasian wild birds: a phylogenetic and phylogeographical study of whole-genome sequence data. <i>Journal of General Virology</i> , 2015, 96, 2050-2060.	1.3	23
18	Whole genome detection of rotavirus mixed infections in human, porcine and bovine samples co-infected with various rotavirus strains collected from sub-Saharan Africa. <i>Infection, Genetics and Evolution</i> , 2015, 31, 321-334.	1.0	42

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19	Global migration of influenza A viruses in swine. <i>Nature Communications</i> , 2015, 6, 6696.	5.8	128
20	The soft palate is an important site of adaptation for transmissible influenza viruses. <i>Nature</i> , 2015, 526, 122-125.	13.7	133
21	Differential Susceptibilities of Human Lung Primary Cells to H1N1 Influenza Viruses. <i>Journal of Virology</i> , 2015, 89, 11935-11944.	1.5	31
22	Phylogenetics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. <i>Journal of Virology</i> , 2015, 89, 8871-8879.	1.5	51
23	Isolation of Type A Influenza Viruses from Red-necked Grebes (<i>Podiceps grisegena</i>). <i>Journal of Wildlife Diseases</i> , 2015, 51, 290-293.	0.3	2
24	Whole genome analyses of G1P[8] rotavirus strains from vaccinated and non-vaccinated South African children presenting with diarrhea. <i>Journal of Medical Virology</i> , 2015, 87, 79-101.	2.5	36
25	The contrasting phylodynamics of human influenza B viruses. <i>ELife</i> , 2015, 4, e05055.	2.8	166
26	Equine Influenza A(H3N8) Virus Isolated from Bactrian Camel, Mongolia. <i>Emerging Infectious Diseases</i> , 2014, 20, 2144-2147.	2.0	42
27	Whole-genome analyses of DS-1-like human G2P[4] and G8P[4] rotavirus strains from Eastern, Western and Southern Africa. <i>Virus Genes</i> , 2014, 49, 196-207.	0.7	29
28	Characterization of Uncultivable Bat Influenza Virus Using a Replicative Synthetic Virus. <i>PLoS Pathogens</i> , 2014, 10, e1004420.	2.1	58
29	Universal Influenza B Virus Genomic Amplification Facilitates Sequencing, Diagnostics, and Reverse Genetics. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1330-1337.	1.8	86
30	Genomic analyses detect Eurasian lineage H10 and additional H14 influenza A viruses recovered from waterfowl in the Central United States. <i>Influenza and Other Respiratory Viruses</i> , 2014, 8, 493-498.	1.5	19
31	Genomewide Analysis of Reassortment and Evolution of Human Influenza A(H3N2) Viruses Circulating between 1968 and 2011. <i>Journal of Virology</i> , 2014, 88, 2844-2857.	1.5	137
32	The evolutionary dynamics of influenza A and B viruses in the tropical city of Managua, Nicaragua. <i>Virology</i> , 2014, 462-463, 81-90.	1.1	6
33	Analysis of Recombinant H7N9 Wild-Type and Mutant Viruses in Pigs Shows that the Q226L Mutation in HA Is Important for Transmission. <i>Journal of Virology</i> , 2014, 88, 8153-8165.	1.5	52
34	Introductions and Evolution of Human-Origin Seasonal Influenza A Viruses in Multinational Swine Populations. <i>Journal of Virology</i> , 2014, 88, 10110-10119.	1.5	88
35	Standards for Sequencing Viral Genomes in the Era of High-Throughput Sequencing. <i>MBio</i> , 2014, 5, e01360-14.	1.8	89
36	North Atlantic Migratory Bird Flyways Provide Routes for Intercontinental Movement of Avian Influenza Viruses. <i>PLoS ONE</i> , 2014, 9, e92075.	1.1	65

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37	Sequencing viral genomes from a single isolated plaque. <i>Virology Journal</i> , 2013, 10, 181.	1.4	16
38	Evolution of a reassortant North American gull influenza virus lineage: drift, shift and stability. <i>Virology Journal</i> , 2013, 10, 179.	1.4	34
39	Synthetic Generation of Influenza Vaccine Viruses for Rapid Response to Pandemics. <i>Science Translational Medicine</i> , 2013, 5, 185ra68.	5.8	164
40	Migration and Persistence of Human Influenza A Viruses, Vietnam, 2001–2008. <i>Emerging Infectious Diseases</i> , 2013, 19, 1756-1765.	2.0	16
41	Avian Influenza: Mixed Infections and Missing Viruses. <i>Viruses</i> , 2013, 5, 1964-1977.	1.5	18
42	Influenza A Virus Migration and Persistence in North American Wild Birds. <i>PLoS Pathogens</i> , 2013, 9, e1003570.	2.1	83
43	Sequence Analysis of <i>In Vivo</i> Defective Interfering-Like RNA of Influenza A H1N1 Pandemic Virus. <i>Journal of Virology</i> , 2013, 87, 8064-8074.	1.5	144
44	Asparagine Substitution at PB2 Residue 701 Enhances the Replication, Pathogenicity, and Transmission of the 2009 Pandemic H1N1 Influenza A Virus. <i>PLoS ONE</i> , 2013, 8, e67616.	1.1	54
45	Antiviral Responses by Swine Primary Bronchoepithelial Cells Are Limited Compared to Human Bronchoepithelial Cells Following Influenza Virus Infection. <i>PLoS ONE</i> , 2013, 8, e70251.	1.1	16
46	Genomic analysis of 16 Colorado human NL63 coronaviruses identifies a new genotype, high sequence diversity in the N-terminal domain of the spike gene and evidence of recombination. <i>Journal of General Virology</i> , 2012, 93, 2387-2398.	1.3	25
47	Engineering temperature sensitive live attenuated influenza vaccines from emerging viruses. <i>Vaccine</i> , 2012, 30, 3691-3702.	1.7	34
48	Genomic reassortment of influenza A virus in North American swine, 1998–2011. <i>Journal of General Virology</i> , 2012, 93, 2584-2589.	1.3	40
49	Influenza A Virus Molecular Virology Techniques. <i>Methods in Molecular Biology</i> , 2012, 865, 175-192.	0.4	82
50	Migratory flyway and geographical distance are barriers to the gene flow of influenza virus among North American birds. <i>Ecology Letters</i> , 2012, 15, 24-33.	3.0	86
51	Reverse genetics plasmid for cloning unstable Influenza A virus gene segments. <i>Journal of Virological Methods</i> , 2011, 173, 378-383.	1.0	19
52	Deep Sequencing Reveals Mixed Infection with 2009 Pandemic Influenza A (H1N1) Virus Strains and the Emergence of Oseltamivir Resistance. <i>Journal of Infectious Diseases</i> , 2011, 203, 168-174.	1.9	113
53	Phylogeography of the Spring and Fall Waves of the H1N1/09 Pandemic Influenza Virus in the United States. <i>Journal of Virology</i> , 2011, 85, 828-834.	1.5	54
54	Extensive Geographical Mixing of 2009 Human H1N1 Influenza A Virus in a Single University Community. <i>Journal of Virology</i> , 2011, 85, 6923-6929.	1.5	43

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55	Temporally structured metapopulation dynamics and persistence of influenza A H3N2 virus in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19359-19364.	3.3	146
56	PB2 Residue 158 Is a Pathogenic Determinant of Pandemic H1N1 and H5 Influenza A Viruses in Mice. <i>Journal of Virology</i> , 2011, 85, 357-365.	1.5	118
57	Unseasonal Transmission of H3N2 Influenza A Virus During the Swine-Origin H1N1 Pandemic. <i>Journal of Virology</i> , 2010, 84, 5715-5718.	1.5	15
58	NS-based live attenuated H1N1 pandemic vaccines protect mice and ferrets. <i>Vaccine</i> , 2010, 28, 8015-8025.	1.7	48
59	Single-Reaction Genomic Amplification Accelerates Sequencing and Vaccine Production for Classical and Swine Origin Human Influenza A Viruses. <i>Journal of Virology</i> , 2009, 83, 10309-10313.	1.5	493
60	Triaryl Pyrazoline Compound Inhibits Flavivirus RNA Replication. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 1320-1329.	1.4	107
61	Mustela Vison ACE2 Functions as a Receptor for Sars-Coronavirus. <i>Advances in Experimental Medicine and Biology</i> , 2006, 581, 507-510.	0.8	12
62	Increased Viral Titers and Subtle Changes in Plaque Morphology Upon Passage of SARS-CoV in Cells from Different Species. <i>Advances in Experimental Medicine and Biology</i> , 2006, 581, 259-263.	0.8	3
63	Analysis of SARS-CoV Receptor Activity of ACE2 Orthologs. <i>Advances in Experimental Medicine and Biology</i> , 2006, 581, 277-280.	0.8	5
64	Cells of human aminopeptidase N (CD13) transgenic mice are infected by human coronavirus-229E in vitro, but not in vivo. <i>Virology</i> , 2005, 335, 185-197.	1.1	35
65	Discovery of Novel Human and Animal Cells Infected by the Severe Acute Respiratory Syndrome Coronavirus by Replication-Specific Multiplex Reverse Transcription-PCR. <i>Journal of Clinical Microbiology</i> , 2004, 42, 3196-3206.	1.8	85
66	CD209L (L-SIGN) is a receptor for severe acute respiratory syndrome coronavirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15748-15753.	3.3	536
67	Identification of a Receptor-Binding Domain of the Spike Glycoprotein of Human Coronavirus HCoV-229E. <i>Journal of Virology</i> , 2003, 77, 2530-2538.	1.5	170
68	Molecular Determinants of Species Specificity in the Coronavirus Receptor Aminopeptidase N (CD13): Influence of N-Linked Glycosylation. <i>Journal of Virology</i> , 2001, 75, 9741-9752.	1.5	102